



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/938,703A

Source:

1600

Date Processed by STIC:

10/29/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

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RAW SEQUENCE LISTING

DATE: 10/29/2003

PATENT APPLICATION: US/09/938,703A

TIME: 15:11:12

Input Set : A:\2023d.ST25.txt

Output Set: N:\CRF4\10292003\I938703A.raw

Does Not Comply
Corrected Diskette Needed

pp 6-7

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Input Set : A:\2023d.ST25.txt

Output Set: N:\CRF4\10292003\I938703A.raw

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73 <222> LOCATION: (1377)..(1377)
74 <223> OTHER INFORMATION: Any nucleotide
77 <220> FEATURE:
78 <221> NAME/KEY: misc_feature
79 <222> LOCATION: (1384)..(1385)
80 <223> OTHER INFORMATION: Any nucleotide
83 <400> SEQUENCE: 2
84 gaattccccc aacagagcca agctctccat ctagtggaca gggaagctag cagcaaacct      60
86 tcccttcact acaaaacttc attgcttggc caaaaagaga gttaattcaa ttagacatc      120
88 tatgtaggca attaaaaacc tattgatgta taaaacagtt tgcattcatg gagggcaact      180
90 aaatacattc taggacttta taaaagatca ctttttattt atgcacaggg tggaaacaaga      240
92 tggattatca agtgtcaagt ccaatctatg acatcaatta ttatacatcg gagccctgcc      300
94 aaaaaatcaa tgtgaagcaa atcgagccc gcctcctgcc tccgctctac tcaactggtg      360
96 tcatctttgg tttgtgggc aacatgctgg tcatcctcat cctgataaac tgcaaaaggc      420
98 tgaagagcat gactgacatc tacctgctca acctggccat ctctgacctg ttttccctc      480
100 ttactgtccc cttctgggct cactatgctg ccgcccagtg ggactttgga aatacaatgt      540
102 gtcaactctt gacagggctc tattttatag gcttcttctc tggaatcttc ttcacatcc      600
104 tcctgacaat cgataggtac ctggctgtcg tccatgctgt gtttgcttta aaagccagga      660
106 cggtcacctt tggggtggtg acaagtgtga tcacttgggt ggtggctgtg tttgcgtctc      720
108 tcccaggaat catctttacc agatctcaaa aagaaggtct tcattacacc tgcagctctc      780
110 attttccata cagtcagtat caattctgga agaatttcca gacattaaag atagtcattc      840
112 tggggctggt cctgcccgtg cttgtcatgg tcactgtcta ctcgggaatc ctaaaaactc      900
114 tgcttcggtg tcgaaatgag aagaagaggc acagggtctg gaggcttatc ttcacatca      960
116 tgattgttta ttttctcttc tgggctccct acaacattgt ccttctcctg aacaccttc      1020
118 aggaattctt tggcctgaat aattgcagta gctctaacag gttggaccaa gctatgcagg      1080
120 tgacagagac tcttgggatg acgcactgct gcacacccc catcatctat gcctttgtcg      1140
122 gggagaagtt cagaaactac ctcttagtct tcttccaaaa gcacattgcc aaacgcttct      1200
124 gcaaatgctg ttctattttc cagcaagagg ctcccagagc agcaagctca gtttacaccc      1260
126 gatccactgg ggagcaggaa atatctgtgg gcttgtgaca cggactcaag tgggctggtg      1320
W--> 128 acccagtcag agttgtgcac atggcttagt tttcatacac agcctgggct gggggtnggt      1380
130 tggnnagagt cttttttaa aggaagttac tgttatagag ggtctaagat tcatccattt      1440
132 atttggcatc tgtttaaagt agattagatc cgaattc      1477
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136 <211> LENGTH: 1442
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 3
141 gaattccccc aacagagcca agctctccat ctagtggaca gggaagctag cagcaaacct      60
143 tcccttcact acaaaacttc attgcttggc caaaaagaga gttaattcaa ttagacatc      120
145 tatgtaggca attaaaaacc tattgatgta taaaacagtt tgcattcatg gagggcaact      180
147 aaatacattc taggacttta taaaagatca ctttttattt atgcacaggg tggaaacaaga      240
149 tggattatca agtgtcaagt ccaatctatg acatcaatta ttatacatcg gagccctgcc      300
151 aaaaaatcaa tgtgaagcaa atcgagccc gcctcctgcc tccgctctac tcaactggtg      360
153 tcatctttgg tttgtgggc aacatgctgg tcatcctcat cctgataaac tgcaaaaggc      420
155 tgaagagcat gactgacatc tacctgctca acctggccat ctctgacctg ttttccctc      480
157 ttactgtccc cttctgggct cactatgctg ccgcccagtg ggactttgga aatacaatgt      540
159 gtcaactctt gacagggctc tattttatag gcttcttctc tggaatcttc ttcacatcc      600
161 tcctgacaat cgataggtac ctggctgtcg tccatgctgt gtttgcttta aaagccagga      660
163 cggtcacctt tggggtggtg acaagtgtga tcacttgggt ggtggctgtg tttgcgtctc      720

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Input Set : A:\2023d.ST25.txt

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165 tcccaggaat catctttacc agatctcaaa aagaaggctc tcattacacc tgcagctctc 780
167 attttccata cattaaagat agtcatcttg gggctgggcc tgccgctgct tgtcatgggc 840
169 atctgtact cgggaatcct aaaaactctg cttcgggtgc gaaatgagaa gaagaggcac 900
171 agggctgtga ggcttatctt caccatcatg attgtttatt ttctcttctg ggctccctac 960
173 aacattgtcc ttctcctgaa caccttccag gaattctttg gcctgaataa ttgcagtagc 1020
175 tctaacaggt tggaccaagc tatgcagggt acagagactc ttgggatgac gcaactgctgc 1080
177 atcaacccca tcatctatgc ctttgtcggg gagaagttca gaaactacct cttagtcttc 1140
179 ttccaaaagc acattgccaa acgcttctgc aaatgctgtt ctattttcca gcaagaggct 1200
181 cccgagcgag caagctcagt ttacacccga tccactgggg agcaggaaaat atctgtgggc 1260
183 ttgtgacacg gactcaagtg ggctgggtgc ccagtcagag ttgtgcacat ggcttagttt 1320
185 tcatacacag cctgggctgg ggggtggttg gaggtctttt ttaaaaggaa gttactgtta 1380
187 tagagggtct aagattcatc catttatttg gcactgtgtt aaagtagatt agatccgaat 1440
189 tc 1442

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192 <210> SEQ ID NO: 4

193 <211> LENGTH: 184

194 <212> TYPE: PRT

195 <213> ORGANISM: Homo sapiens

197 <400> SEQUENCE: 4

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199 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
200 1 5 10 15
203 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
204 20 25 30
207 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
208 35 40 45
211 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
212 50 55 60
215 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
216 65 70 75 80
219 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
220 85 90 95
223 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
224 100 105 110
227 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
228 115 120 125
231 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
232 130 135 140
235 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
236 145 150 155 160
239 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
240 165 170 175
243 Thr Cys Ser Ser His Phe Pro Tyr
244 180

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247 <210> SEQ ID NO: 5

248 <211> LENGTH: 352

249 <212> TYPE: PRT

250 <213> ORGANISM: Homo sapiens

252 <400> SEQUENCE: 5

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254 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
255 1 5 10 15

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Input Set : A:\2023d.ST25.txt

Output Set: N:\CRF4\10292003\I938703A.raw

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258 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
259          20          25          30
262 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
263          35          40          45
266 Met Leu Val Ile Leu Ile Leu Asn Cys Lys Arg Leu Lys Ser Met
267          50          55          60
270 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
271 65          70          75          80
274 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
275          85          90          95
278 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
279          100         105         110
282 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
283          115         120         125
286 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
287          130         135         140
290 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
291 145         150         155         160
294 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
295          165         170         175
298 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
299          180         185         190
302 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
303          195         200         205
306 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
307          210         215         220
310 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
311 225         230         235         240
314 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
315          245         250         255
318 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
319          260         265         270
322 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
323          275         280         285
326 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
327          290         295         300
330 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
331 305         310         315         320
334 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
335          325         330         335
338 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
339          340         345         350
342 <210> SEQ ID NO: 6
343 <211> LENGTH: 215
344 <212> TYPE: PRT
345 <213> ORGANISM: Homo sapiens
347 <400> SEQUENCE: 6
349 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
350 1          5          10          15

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353 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
354          20          25          30
357 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
358          35          40          45
361 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
362          50          55          60
365 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
366 65          70          75          80
369 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
370          85          90          95
373 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
374          100         105         110
377 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
378          115         120         125
381 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
382          130         135         140
385 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
386 145         150         155         160
389 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
390          165         170         175
393 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
394          180         185         190
397 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
398          195         200         205
401 Asn Ser Ala Ser Val Ser Lys
402          210         215
405 <210> SEQ ID NO: 7
406 <211> LENGTH: 360
407 <212> TYPE: PRT
408 <213> ORGANISM: Homo sapiens
410 <220> FEATURE:
411 <221> NAME/KEY: MISC_FEATURE
412 <222> LOCATION: (325)..(327)
413 <223> OTHER INFORMATION: Xaa = any amino acid
416 <400> SEQUENCE: 7
418 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
419 1          5          10          15
422 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
423          20          25          30
426 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
427          35          40          45
430 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
431          50          55          60
434 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
435 65          70          75          80
438 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ile Thr Leu Pro
439          85          90          95
442 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
443          100         105         110

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<210> SEQ ID NO 14
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: :
<400> SEQUENCE: 14
tcgaggatcc aagatggatt atcaagt

27

<210> SEQ ID NO 15
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: :
<400> SEQUENCE: 15
ctgatctaga gccatgtgca caactct

27

<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: :
<400> SEQUENCE: 16
cctggctgtc gtccatgctg

20

<210> SEQ ID NO 17
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: :
<400> SEQUENCE: 17
ctgatctaga gccatgtgca caactct

27

see p. 7
for error explanation

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/938,703A

DATE: 10/29/2003
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FYI

Input Set : A:\2023d.ST25.txt
Output Set: N:\CRF4\10292003\I938703A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1377,1384,1385
Seq#:7; Xaa Pos. 325,326,327
Seq#:8; Xaa Pos. 231,232,233,333,334,335
Seq#:10; Xaa Pos. 145,146,147,321,322,323

Use of <220> Feature (NEW RULES):

error explanation
Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:14,15,16,17

VERIFICATION SUMMARY

DATE: 10/29/2003

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Input Set : A:\2023d.ST25.txt

Output Set: N:\CRF4\10292003\I938703A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1320
M:341 Repeated in SeqNo=2
L:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:320
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
M:341 Repeated in SeqNo=8
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:144
M:341 Repeated in SeqNo=10
L:889 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:891 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:891 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:891 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:891
L:898 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:900 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:900 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:900 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:900
L:907 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:909 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:909 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:909 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:909
L:916 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:918 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:918 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:918 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:918